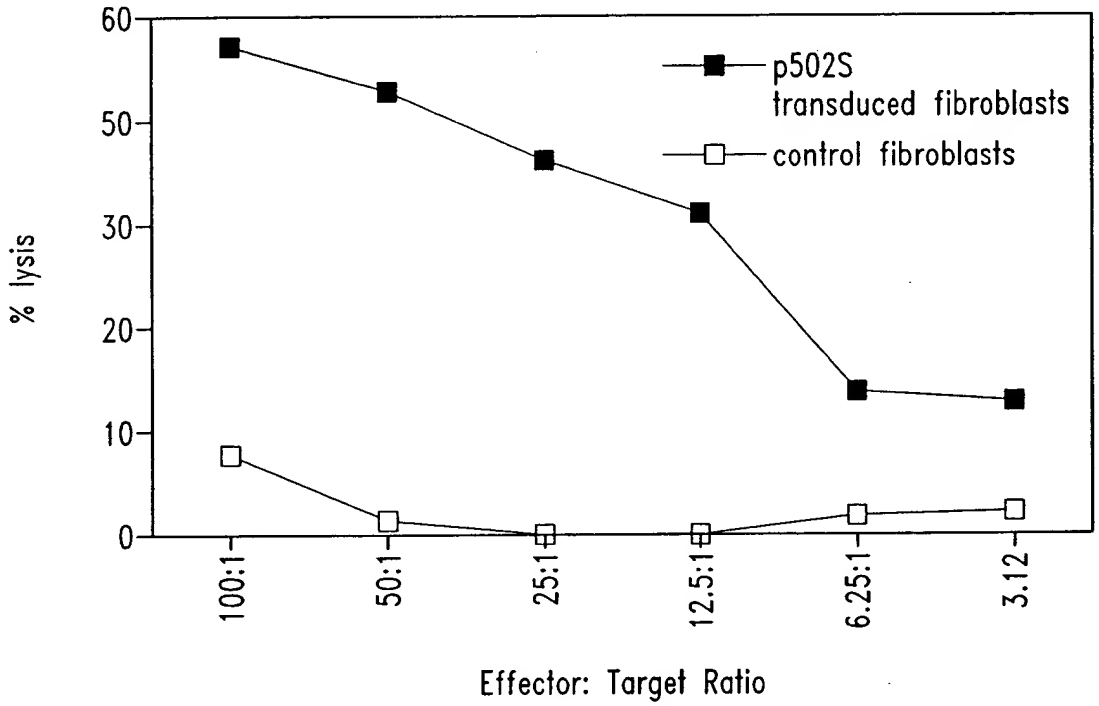

60
50
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1

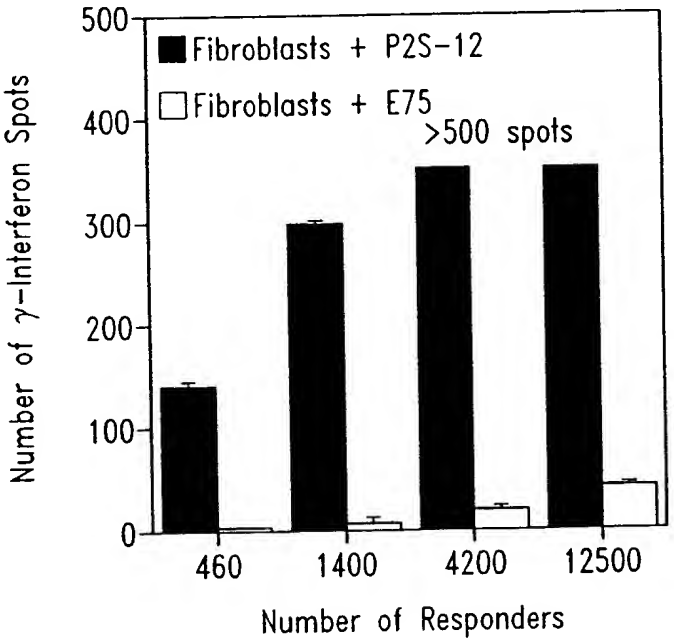

500
400
300
200
100
0
Fibroblasts + P2S-12
Fibroblasts + E75
>500 spots
Number of γ-Interferon Spots
460
1400
4200
12500
Number of Responders

Fig. 2A

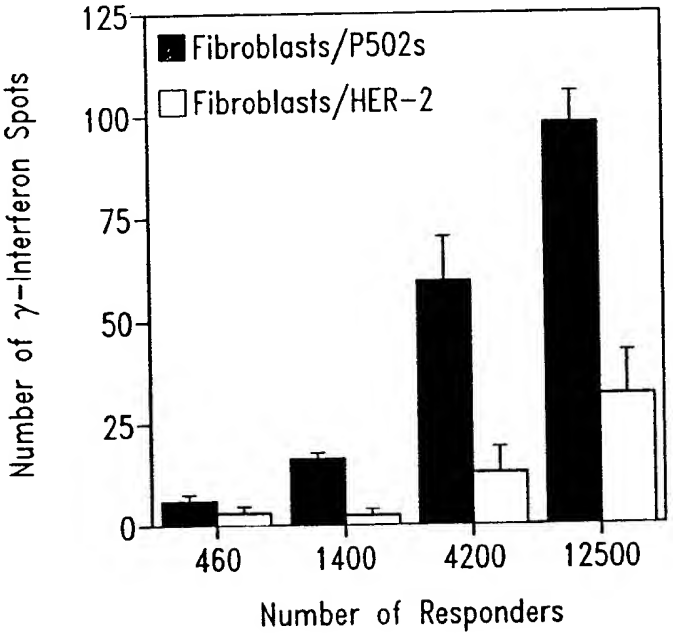

125
100
75
50
25
0
Fibroblasts/P502s
Fibroblasts/HER-2
Number of γ-Interferon Spots
460
1400
4200
12500
Number of Responders

Fig. 2B

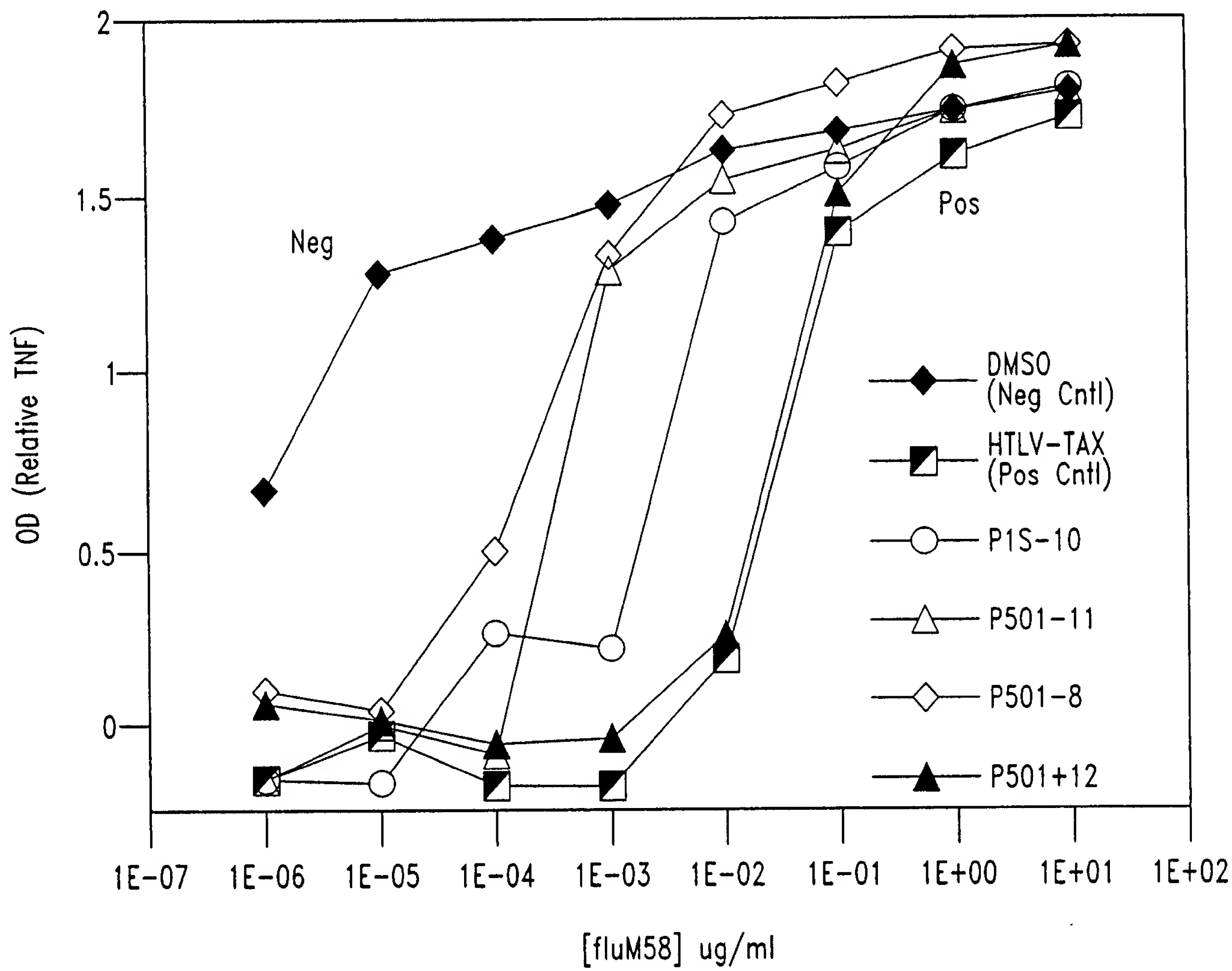

Neg
Pos
DMSO
(Neg Cntl)
HTLV-TAX
(Pos Cntl)
P1S-10
P501-11
P501-8
P501+12
OD (Relative TNF)
2
1.5
1
0.5
0
1E-07
1E-06
1E-05
1E-04
1E-03
1E-02
1E-01
1E+00
1E+01
1E+02
[fluM58] ug/ml

Fig. 3

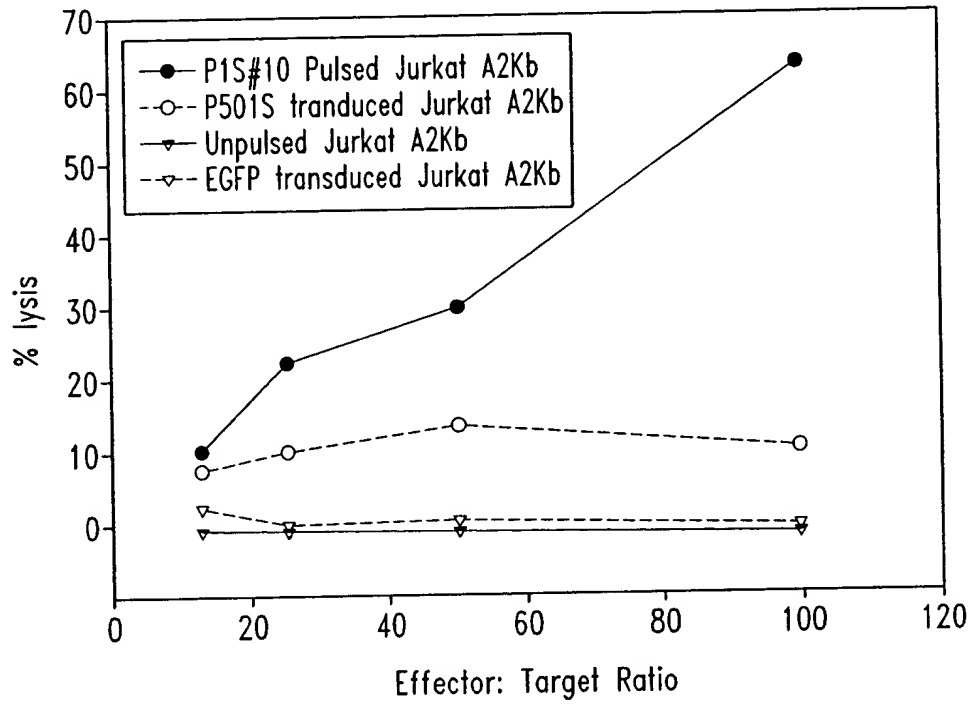

P1S#10 Pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
Unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Fig. 4

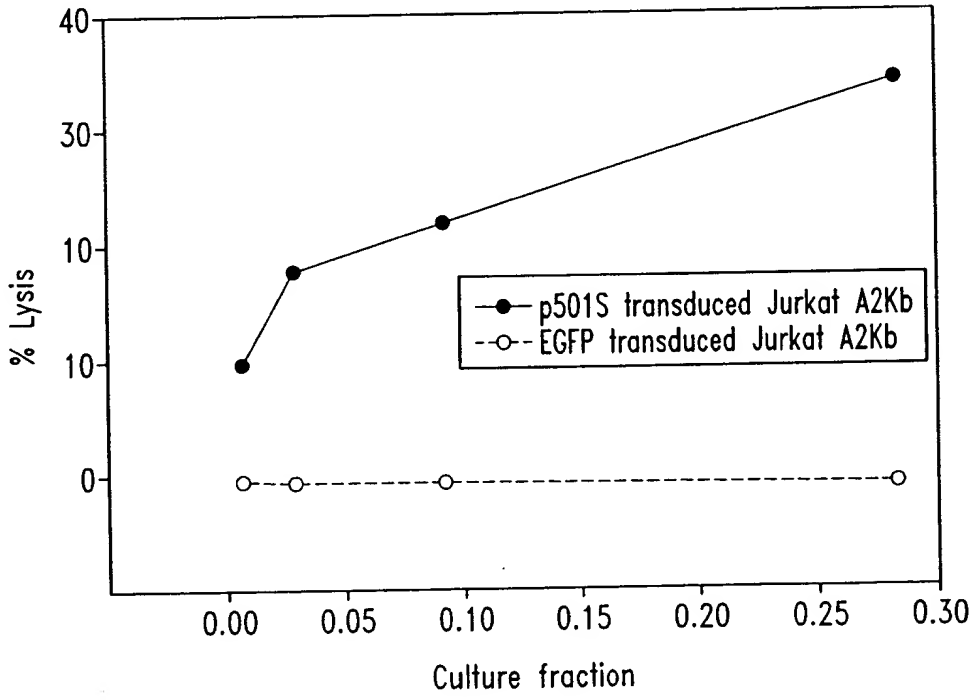

p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% Lysis
Culture fraction
0
10
10
30
40
0.00
0.05
0.10
0.15
0.20
0.25
0.30

Fig. 5

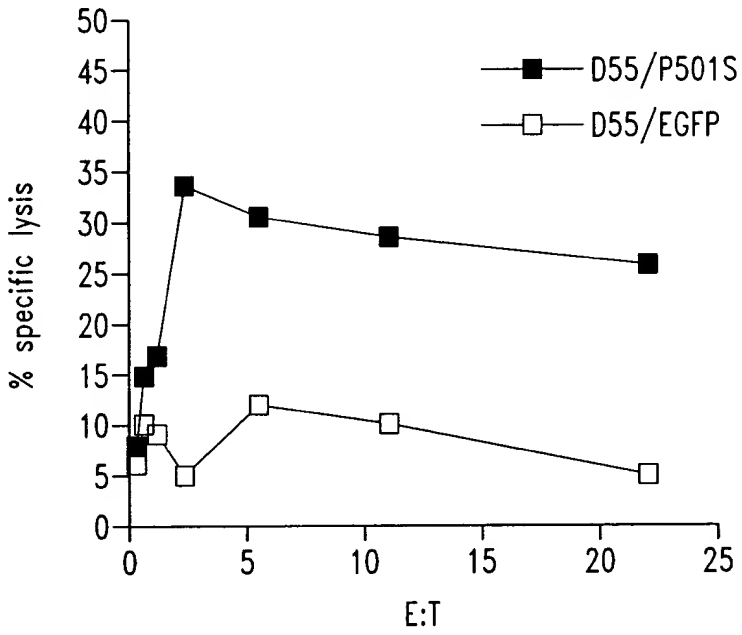

D55/P501S
D55/EGFP
% specific lysis
E:T
0
5
10
15
20
25
30
35
40
45
50

Fig. 6A

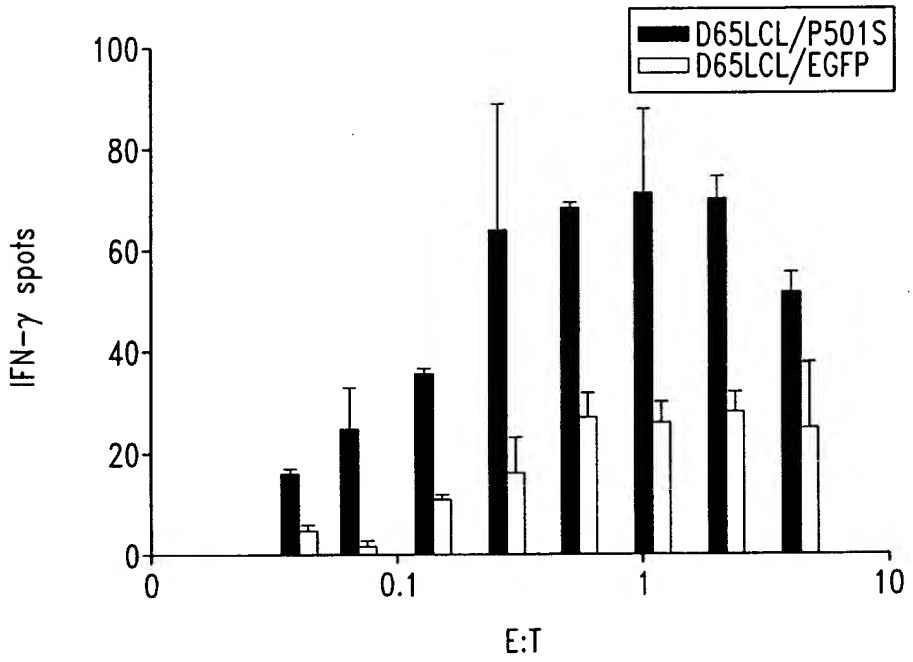
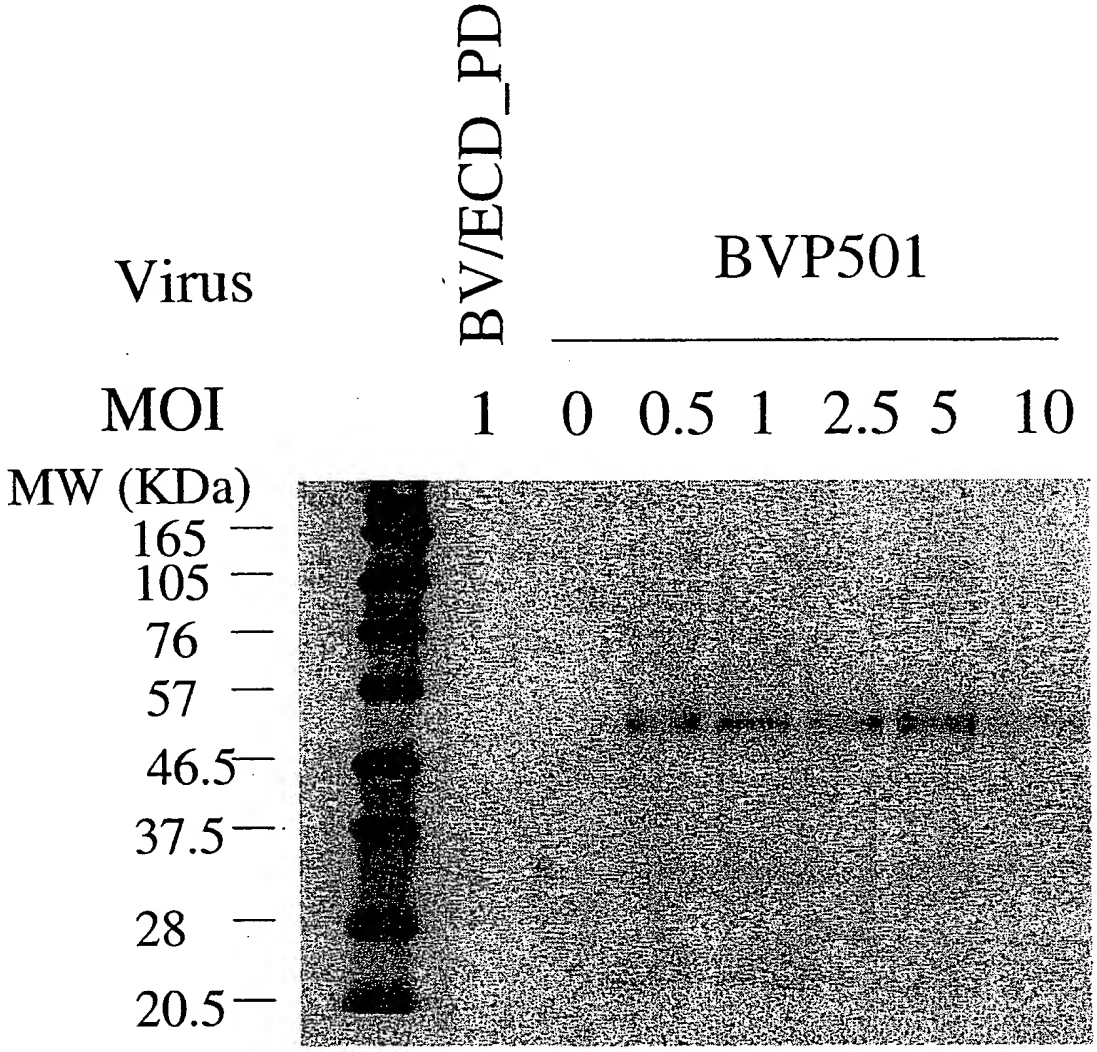

D65LCL/P501S
D65LCL/EGFP
IFN-γ spots
E:T
0
20
40
60
80
100
0
0.1
1
10

Fig. 6B

Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 – 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

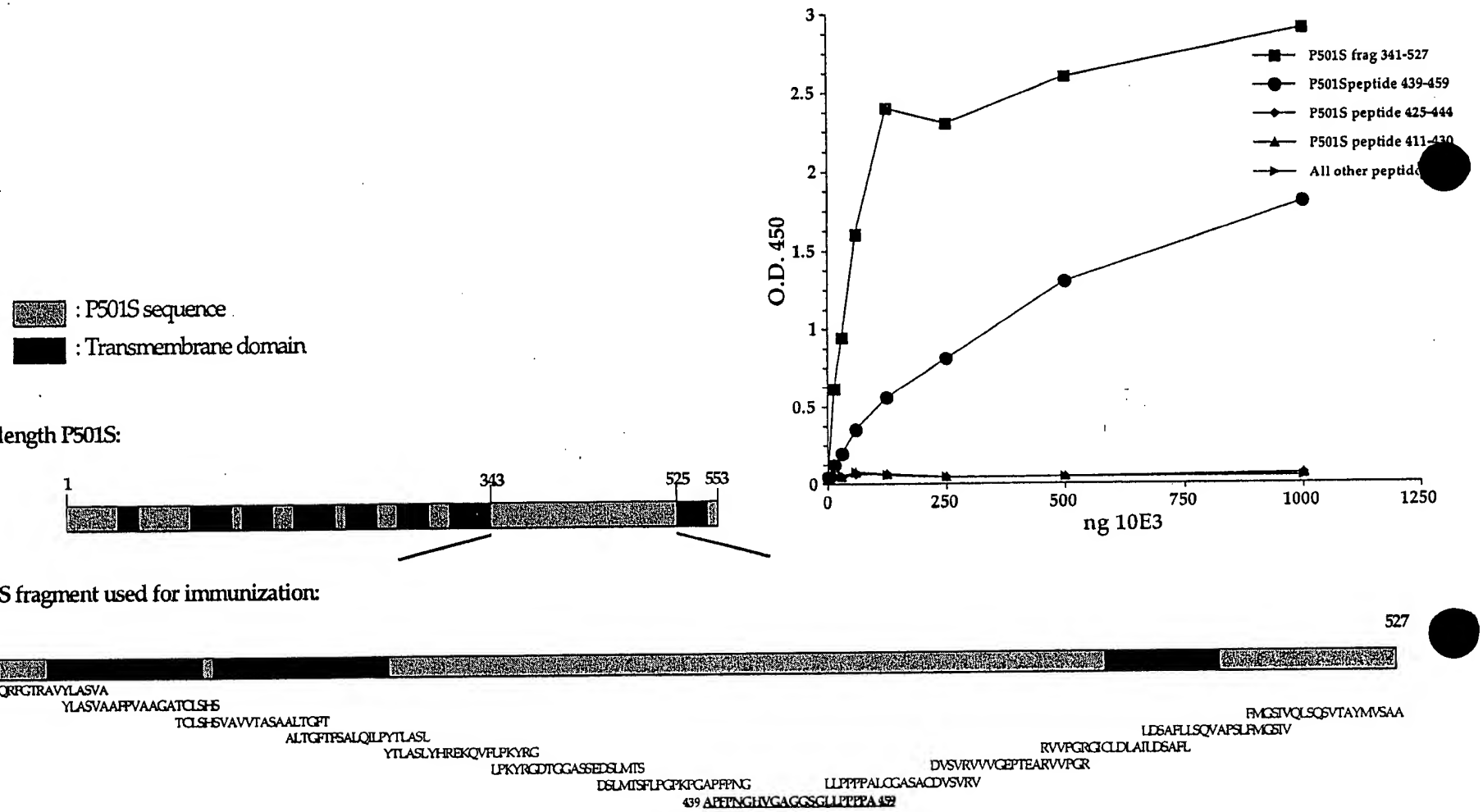


Fig. 8

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLAVVSRLLRIRK AQLLLYNLLTFGLEVCLAAGIT YVPPLLLEVGVEEKFM TMVLGIGPVLGLVCVPLLQSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

FALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWDTSALAPVLGTQFE

CLPGLLTLIFLTCVAATLLV *AEGAATGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGAILPRL*

HQLCCRSIPRTLRR LPVAFLCSWMALMTFTLFYTDP VGEGLYQGVPLAIPGTLAARHIYDEGVL

MQSLGLFLQCAISLVFSLVM *DRLVQREGTRAVYLAS* VAAFPVAAGIATCLSHSVAVYTA SAA

LTGEIFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG LCLDLAILDSAFLLSQVAPSLF MGSIVQLSQS

VTAYMVSAAGLGLVALYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

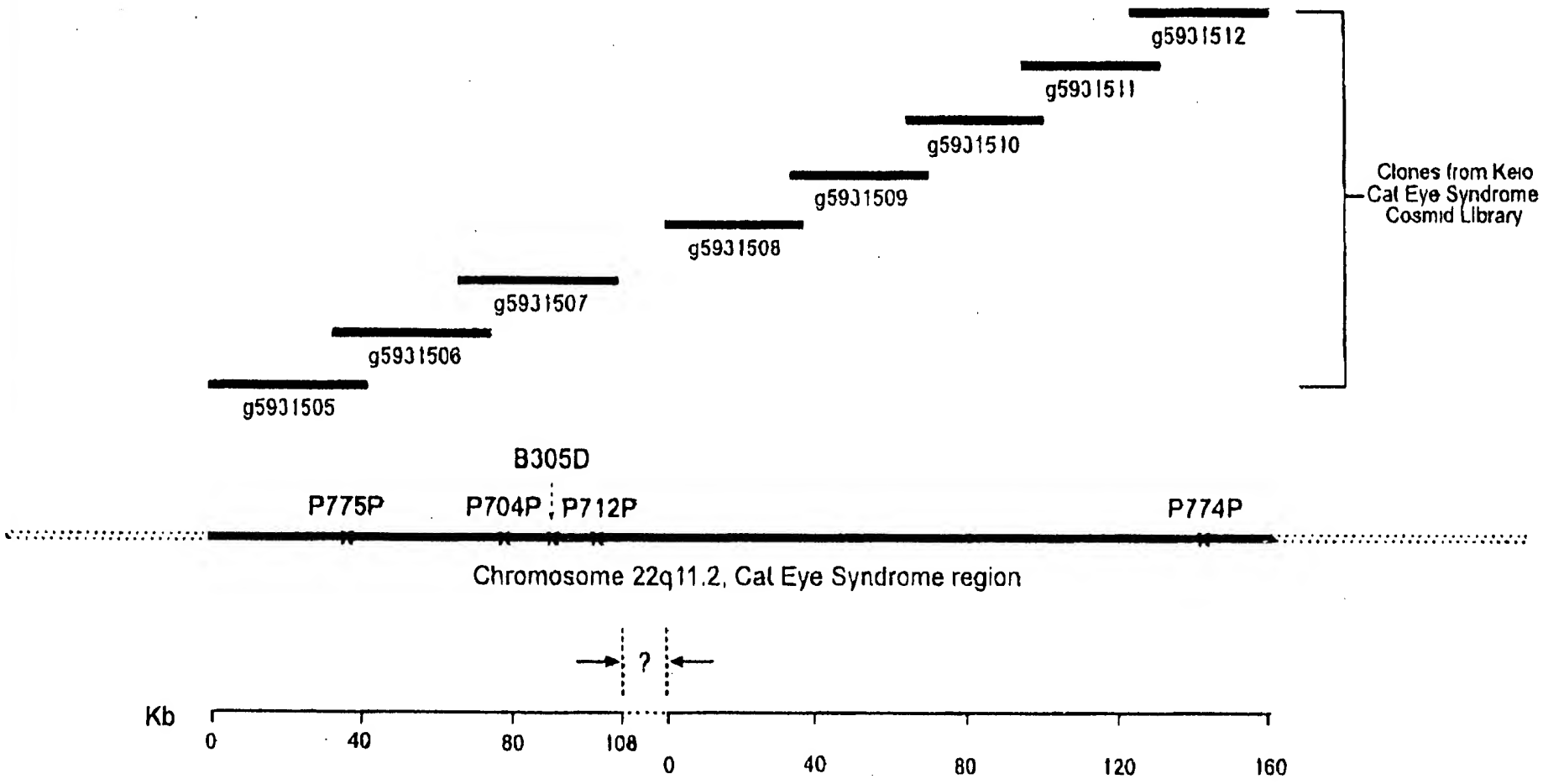


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

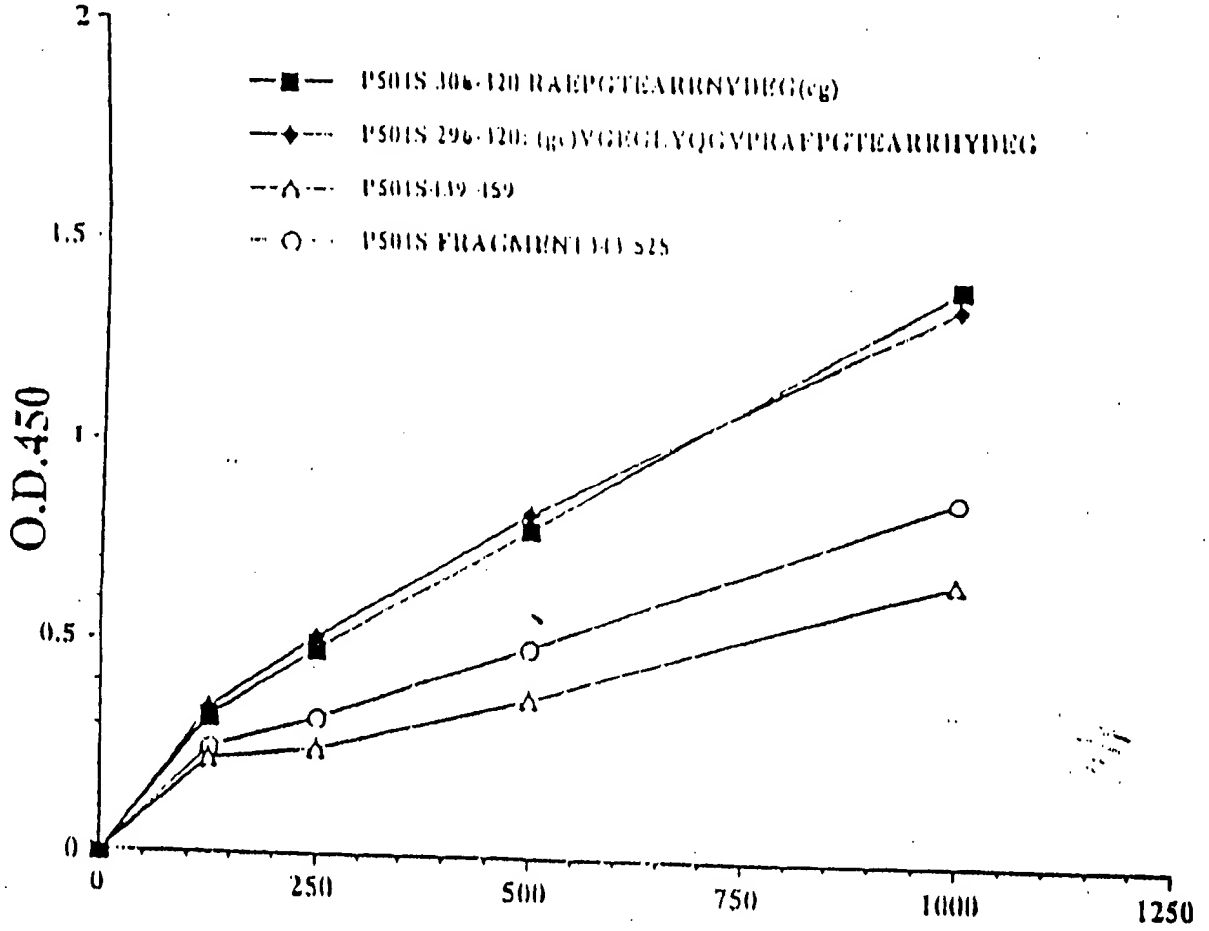
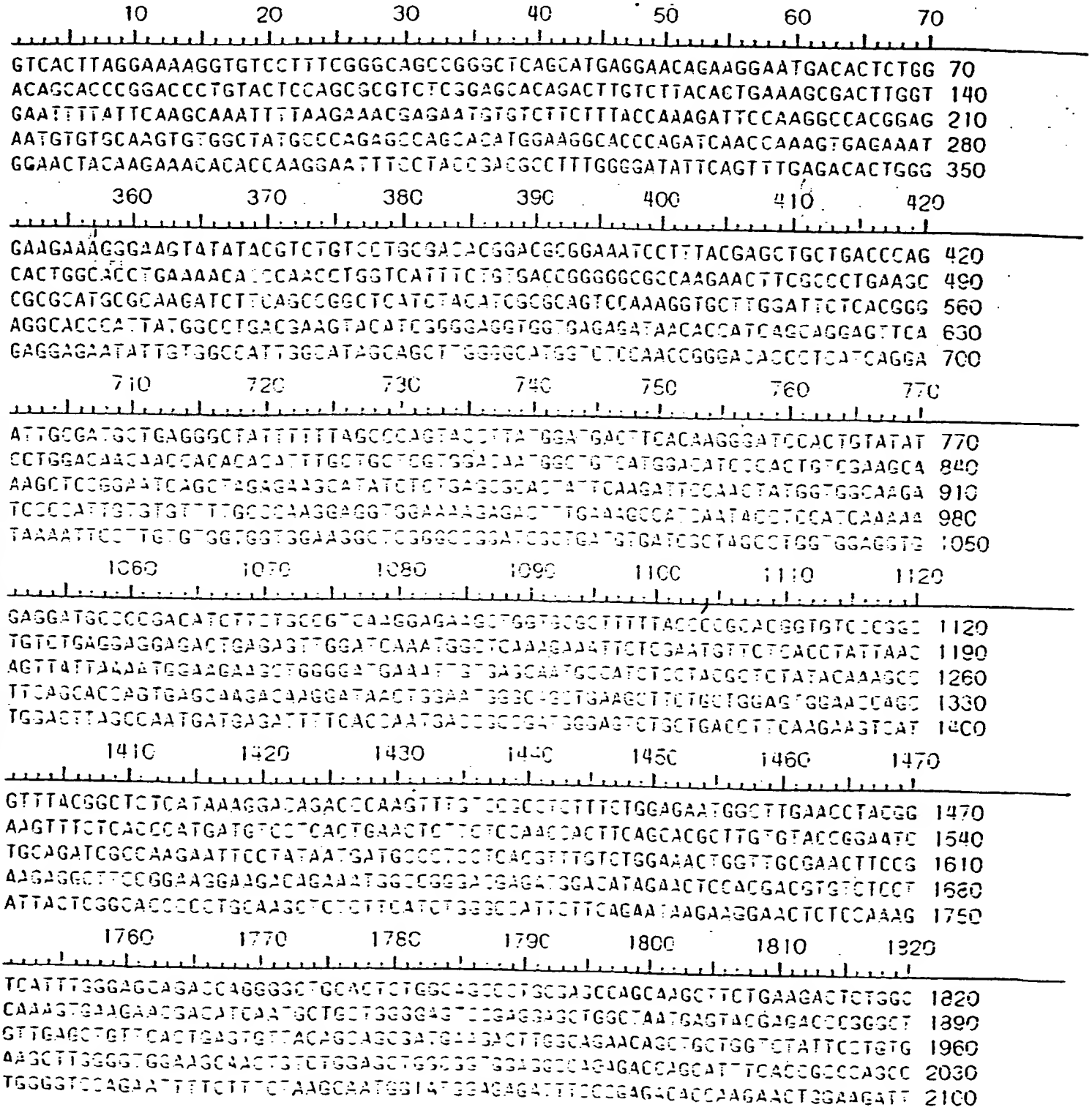


Fig. 11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GAATTTTATTCAAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAACTACAAGAAACACACCAAGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGG 350
360 370 380 390 400 410 420
GAAGAAAGGGAAGTATATACGTCTGTCCTGCGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAG 420
CACTGGCACCTGAAAACATCCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
AGGCACCCATTATGGCCTGACGAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
GAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCTCATCAGGA 700
710 720 730 740 750 760 770
ATTGCGATGCTGAGGGCTATTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGGGATCCACTGTATAT 770
CCTGGACAACAACCACACACATTTGCTGCTGGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCA 840
AAGCTCCGGAATCAGCTAGAGAAGCATATCTCTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGA 910
TCCCCATTGTGTGTTTGCCCAAGGAGGTGGAAAAGAGACTTGAAGCCATCAATACCTCCATCAAAAA 980
TAAAATTCCTTGTGTGGTGGAAGGCTCGGGCCGGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTG 1050
1060 1070 1080 1090 1100 1110 1120
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TGTCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTCTCGAATGTTCTCACCTATTAAC 1190
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1410 1420 1430 1440 1450 1460 1470
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1760 1770 1780 1790 1800 1810 1820
TCATTTGGGAGCAGACCAGGGGCTGCACTCTGGCAGCCCTGCGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820
CAAAGTGAAGAACGACATCAATGCTGCTGGGGAGTCCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCT 1890
GTTGAGCTGTTCACTGAGTGTTACAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCCTGTG 1960
AAGCTTGGGGTGGAAGCAACTGTCTGGAGCTGGCGGTGGAGGCCAGAGACCAGCATTTCACCGCCCAGCC 2030
TGGGGTCCAGAATTTTCTTTCTAAGCAATGGTATGGAGAGATTTCCGAGACACCAAGAACTGGAAGATT 2100

Fig. 12A (1)


2110 2120 2130 2140 2150 2160 2170
TCCTGTGTCTGTTTATTATACCTTGGTGGGCTGTGGCTTTGTATCATTTAGGAAAAACCTGTCGACA 2170
AGCACAAGAAGCTGCTTTGGTACTATGTGGGGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGT 2240
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CCCCCCGAGCTGCTCCTGTACTCCCTGGTCTTTGTCCTCTTCTGTGATGAAGTCAGACAGTGGTACGTAA 2380
ATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTTTACTTCATAGCAGG 2450
2460 2470 2480 2490 2500 2510 2520
AATTGTATTTCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTCTGGAC 2520
TACATTATTTTCACTCTAAGATTGATCCACATTTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590
TGCTGCAGAGGATGCTGATCGATGTGTTCTTGTTCCTGTTCCTCTTTGCGGTGTGGATGGTGGCCTTTGG 2660
CGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCCGTTCGGTCATCTAC 2730
GAGCCCTACCTGGCCATGTTCGGCCAGGTGCCGAGTGACGTGGATGGTACCACGTATGACTTTGCCCACT 2800
2810 2820 2830 2840 2850 2860 2870
GCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCCGGTTCCC 2870
CGAGTGGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTG 2940
GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGT 3010
ACTTCCTGGTGCAGGAGTACTGCAGCCGCTTCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTA 3080
CATGGTGGTGAAGAAGTCCTTCAAGTGTTGCTGCAAGGAGAAAAACATGGAGTCTTCTGTCTGCTGTTTC 3150
3160 3170 3180 3190 3200 3210 3220
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CAAGGGTCTTCTGAAAGAGATTGCTAATAAAATCAAATAAAACTGTATGAAACTCTAATGGAGAAAAATC 3360
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3510 3520 3530 3540 3550 3560 3570
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TTTTTCCTTTAATCTTATTTTTGATGAACACATATATAGGAGAACATCTATCCTATGAATAAGAACCTGG 3710
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3860 3870 3880 3890 3900 3910 3920
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4210 4220 4230 4240 4250 4260 4270
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ATTCCAATAAATATCTATTTATTATTAAATATTAAAATATCGATTTATTATTAAAACCATTTATAAGGCT 4550

Fig. 12A(2)

4560 4570 4580 4590 4600 4610 4620

TTTTCATAAATGTATAGCAAATA[redacted]AATTATTAACTTGAGCATAAGATATGAGAT[redacted]ATGAACCTGAACT 4620
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GGTGGGCAGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACCACATCTCTACT 4760
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AAGAATTGCTGGAACCTGGGAGGCGGAGGTTGCAGTGAACCAAGATTGCACCACTGCACTCCAGCCGGGG 4900

4910 4920 4930 4940 4950 4960 4970

TGACAGAGTGAGACTCCGACTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATATTATGG 4970
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5260 5270 5280 5290 5300 5310 5320

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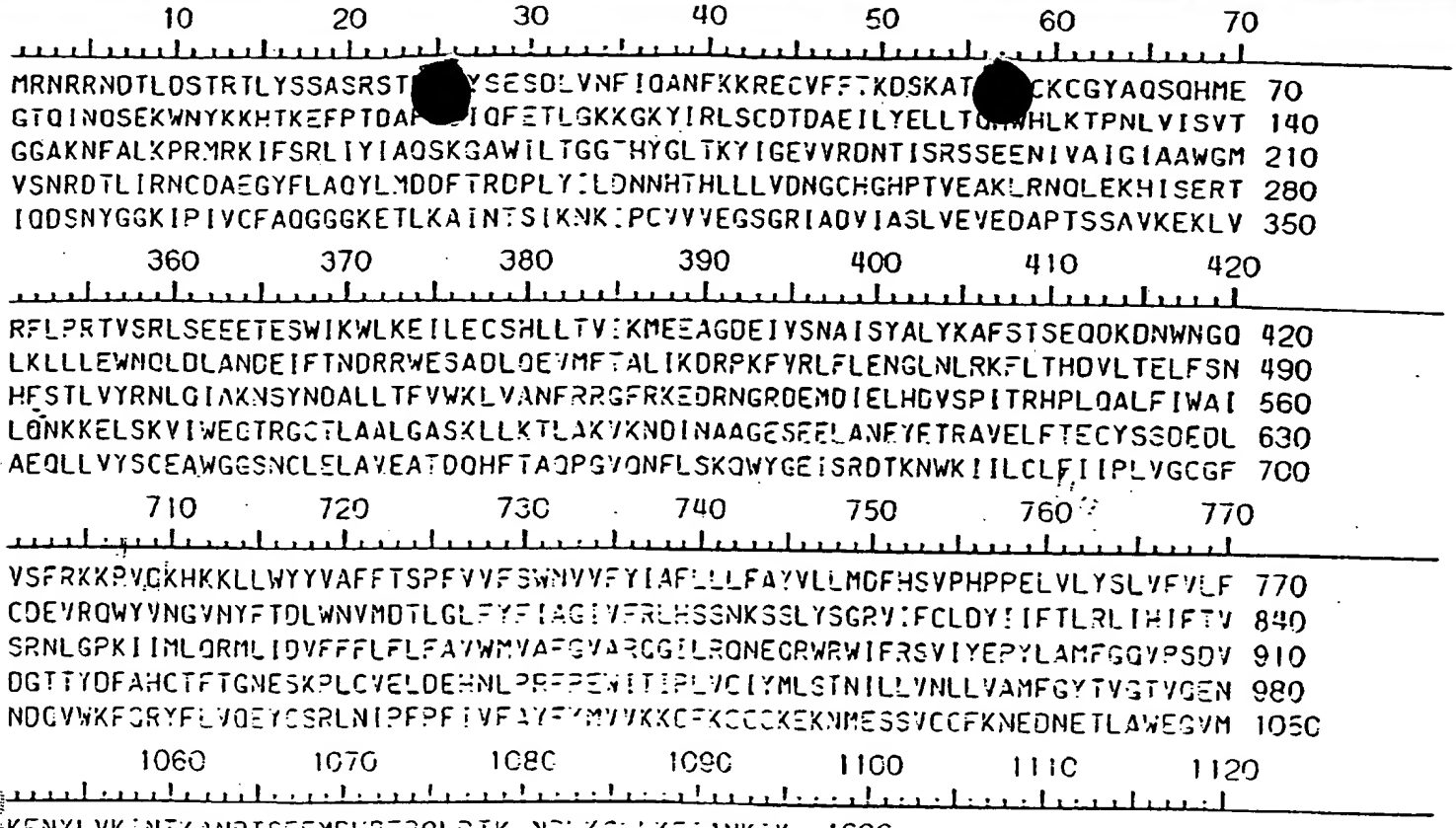
5610 5620 5630 5640 5650 5660 5670

GTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5668

Fig. 12A(3)

15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VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT 280
IQDSNYGGKIPIVCFAQGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV 350
360 370 380 390 400 410 420
RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQQKDNWNGQ 420
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN 490
HFSTLVYRNLQIAKNSYNQALLTFVWKLVANFRRGFRKEDRNGRQEMDIELHQVSPITRHPLQALFIWAI 560
LQNKKELSKVIWEGTRGGTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSQEDL 630
AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISRDTKNWKIILCLFIIPLVGCGF 700
710 720 730 740 750 760 770
VSFRKKPVGKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLLMQFHSVPHPPELVLYSLVFVLF 770
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1060 1070 1080 1090 1100 1110 1120
GKENYLVKINTKANDTSEEMRHRFRQLDTKLNDLKGLLKEIANKIK. 1096

Fig. 12B